12-Distribution in the *Musa* diversity of two large chromosomal translocations using re-sequencing data.

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Banana cultivars are derived from hybridization between *Musa acuminata* subspecies. Theses subspecies diverged following geographical isolation in distinct Southeast Asian continental regions and islands. Observation of chromosome pairing irregularities in meiosis of hybrids between theses subspecies suggested the presence of large chromosomal structural variations (LSV). We recently described a reciprocal translocation compare to the sequence *M. acuminata* reference in a subgroup of *malaccensis* accessions and another one in *M. balbisiana*.

Using a self-progeny of Calcutta4 genotyped by GBS and large insert paired reads mapped on the reference genome, we characterized two large structural variations in the accession "Calcutta4" from the subspecies *burmannicoides* relative to the reference sequence assembly obtained with a *M. a.* ssp *malaccensis* accession. These large structural variations consist in a reciprocal translocation involving a 240 kb distal region of acrocentric chromosome 2 and a 7.2 Mb distal region of chromosome 8 and a second reciprocal translocation involving a 20.8Mb distal region of acrocentric chromosome 1 and an 11.6Mb distal region of chromosome 9. At the breakpoints, intricate events of duplication and deletion/rearrangements involving small fragments were detected. These rearrangement were validated using a preliminary assembly of "Calcutta 4" accession obtained from Nanopore Reads.

We developed a methodology to exploit short-insert paired reads resequencing data to analyze the distribution of these two LSV in Musa germplasm. To do so, we designed a pipeline looking for read pair overlapping rearrangement breakpoints for the two structures. First results suggested micro-variations at rearrangement breakpoints for several representatives of *Musa acuminata* diversity. We thus used PacBio and Nanopore sequencing data from 2 additional representatives of *Musa acuminata* subspecies (ssp *banksii* and ssp *zebrina*) to design additional rearrangement breakpoints for these accessions. All breakpoints presence/absence where then tested for the 159 accessions for which paired reads were available.

Results showed that both translocations are shared by all wild accessions belonging to the *burmannicoides/burmannica/siamea* subspecies. The chromosome 2/8 translocation is also found at the heterozygous state in two cultivars. The relatively low frequency in cultivated accessions of these alternate structures confirmed that *burmannicoides/burmannica/siamea* subspecies had a low contribution to cultivated bananas. Those two *M. a. burmannica* specific large structural variations correspond to the "Northern" group suggested by Shepherd (1999) based on meiosis observations.